#3

OIPE

RAW SEQUENCE LISTING   DATE: 02/06/2001
PATENT APPLICATION: US/09/770,509   TIME: 15:23:09

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\02062001\I770509.raw

```
       4 <110> APPLICANT: Katagiri, F.
       6 <120> TITLE OF INVENTION: OOMYCETE FTSZ-MT AS A TARGET FOR
       7       ANTIMICROBIAL-SPECIFIC BIOCIDES
      10 <130> FILE REFERENCE: NADII.018A
C-->  12 <140> CURRENT APPLICATION NUMBER: US/09/770,509
C-->  12 <141> CURRENT FILING DATE: 2001-01-25
      12 <160> NUMBER OF SEQ ID NOS: 32
      14 <170> SOFTWARE: FastSEQ for Windows Version 4.0
      16 <210> SEQ ID NO: 1
      17 <211> LENGTH: 535
      18 <212> TYPE: DNA
      19 <213> ORGANISM: Phytophthora infestans
      21 <220> FEATURE:
      22 <221> NAME/KEY: CDS
      23 <222> LOCATION: (2)...(535)
      25 <400> SEQUENCE: 1
      26 c gcg tcg caa ttg gaa ggt gtg gag ttc att gta gcc aac aca gac tgt 49
      27   Ala Ser Gln Leu Glu Gly Val Glu Phe Ile Val Ala Asn Thr Asp Cys
      28    1           5                   10                  15
      30 cag gct ctg gga cgc tcg ctg gcg ccg cac aag atc acg ctg ggc aaa    97
      31 Gln Ala Leu Gly Arg Ser Leu Ala Pro His Lys Ile Thr Leu Gly Lys
      32             20                  25                  30
      34 gat atc acc aag gga cta gga gct gga tcc aaa cct gag ctg ggt aaa   145
      35 Asp Ile Thr Lys Gly Leu Gly Ala Gly Ser Lys Pro Glu Leu Gly Lys
      36         35                  40                  45
      38 cgc tct gcg gaa cag cag aaa gtg gat atc caa cgg atg tta cag gac   193
      39 Arg Ser Ala Glu Gln Gln Lys Val Asp Ile Gln Arg Met Leu Gln Asp
      40     50                  55                  60
      42 agc aac atg ctg ttt atc acg ggc gga atg ggc ggc gga acc tgc aca   241
      43 Ser Asn Met Leu Phe Ile Thr Gly Gly Met Gly Gly Gly Thr Cys Thr
      44 65                  70                  75                  80
      46 gga gcc gca cct gtc gtg gcc agt gta gcc agg gag ctg ggg atc cta   289
      47 Gly Ala Ala Pro Val Val Ala Ser Val Ala Arg Glu Leu Gly Ile Leu
      48             85                  90                  95
      50 acg gtc gga gta gta agc aca ccg ttc cga tcc gaa gga ccc aat cgc   337
      51 Thr Val Gly Val Val Ser Thr Pro Phe Arg Ser Glu Gly Pro Asn Arg
      52             100                 105                 110
      54 act cgt ctg gcc aat gct gga gta aaa gaa ctg gcc aag tac gtc gac   385
      55 Thr Arg Leu Ala Asn Ala Gly Val Lys Glu Leu Ala Lys Tyr Val Asp
      56         115                 120                 125
      58 acc tta att gtc gtg ccc aac cag aac ttg ctg gct ttg gca gac aag   433
      59 Thr Leu Ile Val Val Pro Asn Gln Asn Leu Leu Ala Leu Ala Asp Lys
      60     130                 135                 140
      62 agc acg acc atg ttg gaa gcc ttc cgg tat gcc gac gac gtg ctg ctt   481
      63 Ser Thr Thr Met Leu Glu Ala Phe Arg Tyr Ala Asp Asp Val Leu Leu
      64 145                 150                 155                 160
      66 gaa gga gtt aaa ggt gtc acg gac ttg atc gtt cgc ccg gga ctt atc   529
```

```
67 Glu Gly Val Lys Gly Val Thr Asp Leu Ile Val Arg Pro Gly Leu Ile
68               165             170             175
70 aat ttg                                                                535
71 Asn Leu
75 <210> SEQ ID NO: 2
76 <211> LENGTH: 178
77 <212> TYPE: PRT
78 <213> ORGANISM: Phytophthora infestans
80 <400> SEQUENCE: 2
81 Ala Ser Gln Leu Glu Gly Val Glu Phe Ile Val Ala Asn Thr Asp Cys
82  1           5               10              15
83 Gln Ala Leu Gly Arg Ser Leu Ala Pro His Lys Ile Thr Leu Gly Lys
84           20              25              30
85 Asp Ile Thr Lys Gly Leu Gly Ala Gly Ser Lys Pro Glu Leu Gly Lys
86           35              40              45
87 Arg Ser Ala Glu Gln Gln Lys Val Asp Ile Gln Arg Met Leu Gln Asp
88       50              55              60
89 Ser Asn Met Leu Phe Ile Thr Gly Gly Met Gly Gly Gly Thr Cys Thr
90 65              70              75              80
91 Gly Ala Ala Pro Val Val Ala Ser Val Ala Arg Glu Leu Gly Ile Leu
92               85              90              95
93 Thr Val Gly Val Val Ser Thr Pro Phe Arg Ser Glu Gly Pro Asn Arg
94           100             105             110
95 Thr Arg Leu Ala Asn Ala Gly Val Lys Glu Leu Ala Lys Tyr Val Asp
96           115             120             125
97 Thr Leu Ile Val Val Pro Asn Gln Asn Leu Leu Ala Leu Ala Asp Lys
98       130             135             140
99 Ser Thr Thr Met Leu Glu Ala Phe Arg Tyr Ala Asp Asp Val Leu Leu
100 145             150             155             160
101 Glu Gly Val Lys Gly Val Thr Asp Leu Ile Val Arg Pro Gly Leu Ile
102              165             170             175
103 Asn Leu
107 <210> SEQ ID NO: 3
108 <211> LENGTH: 220
109 <212> TYPE: DNA
110 <213> ORGANISM: Phytophthora infestans
112 <220> FEATURE:
113 <221> NAME/KEY: CDS
114 <222> LOCATION: (2)...(220)
115 <223> OTHER INFORMATION: cDNA
117 <400> SEQUENCE: 3
118 c gcg cgc ggc ctg cag ggt gtg gag ttt ctt gtt tgc aac acg gat gct 49
119   Ala Arg Gly Leu Gln Gly Val Glu Phe Leu Val Cys Asn Thr Asp Ala
120   1           5               10              15
122 cag cac tta cgc acg acg ctg acg gag aac cgc gtt cag atg gct cct 97
123 Gln His Leu Arg Thr Thr Leu Thr Glu Asn Arg Val Gln Met Ala Pro
124           20              25              30
126 gaa ttg act gga gga ttg ggc tgt ggc gct aac ccc gaa gtt ggc cga 145
127 Glu Leu Thr Gly Gly Leu Gly Cys Gly Ala Asn Pro Glu Val Gly Arg
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```
128          35                   40                   45
130 gag gcg gca gag gcc gcg att gat gag att ttg gag cgc gtt cag ggt   193
131 Glu Ala Ala Glu Ala Ala Ile Asp Glu Ile Leu Glu Arg Val Gln Gly
132      50                   55                   60
134 gca aac atg atg ttt gtt act gcg ggt                              220
135 Ala Asn Met Met Phe Val Thr Ala Gly
136 65                   70
139 <210> SEQ ID NO: 4
140 <211> LENGTH: 73
141 <212> TYPE: PRT
142 <213> ORGANISM: Phytophthora infestans
144 <400> SEQUENCE: 4
145 Ala Arg Gly Leu Gln Gly Val Glu Phe Leu Val Cys Asn Thr Asp Ala
146  1           5                   10                  15
147 Gln His Leu Arg Thr Thr Leu Thr Glu Asn Arg Val Gln Met Ala Pro
148           20                  25                  30
149 Glu Leu Thr Gly Gly Leu Gly Cys Gly Ala Asn Pro Glu Val Gly Arg
150           35                  40                  45
151 Glu Ala Ala Glu Ala Ala Ile Asp Glu Ile Leu Glu Arg Val Gln Gly
152      50                   55                   60
153 Ala Asn Met Met Phe Val Thr Ala Gly
154 65                   70
157 <210> SEQ ID NO: 5
158 <211> LENGTH: 388
159 <212> TYPE: DNA
160 <213> ORGANISM: Phytophthora infestans
162 <220> FEATURE:
163 <221> NAME/KEY: intron
164 <222> LOCATION: (143)...(204)
166 <221> NAME/KEY: intron
167 <222> LOCATION: (265)...(370)
169 <221> NAME/KEY: CDS
170 <222> LOCATION: (2)...(142)
172 <221> NAME/KEY: CDS
173 <222> LOCATION: (205)...(264)
175 <221> NAME/KEY: CDS
176 <222> LOCATION: (371)...(388)
178 <400> SEQUENCE: 5
179 c gcg cgc ggc ctg cag ggt gtg gag ttt ctt gtt tgc aac acg gat gct 49
180   Ala Arg Gly Leu Gln Gly Val Glu Phe Leu Val Cys Asn Thr Asp Ala
181    1           5                   10                  15
183 cag cac tta cgc acg acg ctg acg gag aac cgc gtt cag atg gct cct   97
184 Gln His Leu Arg Thr Thr Leu Thr Glu Asn Arg Val Gln Met Ala Pro
185           20                  25                  30
187 gaa ttg act gga gga ttg ggc tgt ggc gct aac ccc gaa gtt ggg       142
188 Glu Leu Thr Gly Gly Leu Gly Cys Gly Ala Asn Pro Glu Val Gly
189           35                  40                  45
191 tgagtgactg cgtaaaagcg gtattttttt ttcttacata ctgaccttaa ctattgatta 202
192 gc cga gag gcg gca gag gcc gcg att gat gag att ttg gag cgc gtt    249
```

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```
193    Arg Glu Ala Ala Glu Ala Ala Ile Asp Glu Ile Leu Glu Arg Val
194             50                  55                  60
196 cag ggt gca aac atg gtttgtctcg gtgacattgc gtttctcaag acgttccgat    304
197 Gln Gly Ala Asn Met
198           65
200 ttgagcgaat gacttggtga tgacaacgat atgattatta acttctgctt ttatgcccct 364
201 atatag atg ttt gtt act gcg ggt                                    388
202         Met Phe Val Thr Ala Gly
203                     70
206 <210> SEQ ID NO: 6
207 <211> LENGTH: 20
208 <212> TYPE: DNA
209 <213> ORGANISM: Artificial Sequence
211 <220> FEATURE:
212 <223> OTHER INFORMATION: PCR primer
215 <221> NAME/KEY: misc_feature
216 <222> LOCATION: (1)...(20)
217 <223> OTHER INFORMATION: n = inosine
219 <400> SEQUENCE: 6
W--> 220 aaygcngtna ayaayatgat                                        20
222 <210> SEQ ID NO: 7
223 <211> LENGTH: 20
224 <212> TYPE: DNA
225 <213> ORGANISM: Artificial Sequence
227 <220> FEATURE:
228 <223> OTHER INFORMATION: PCR primer
231 <221> NAME/KEY: misc_feature
232 <222> LOCATION: (1)...(20)
233 <223> OTHER INFORMATION: n = inosine
235 <400> SEQUENCE: 7
W--> 236 gtnccngtnc cnccncccat                                        20
238 <210> SEQ ID NO: 8
239 <211> LENGTH: 20
240 <212> TYPE: DNA
241 <213> ORGANISM: Artificial Sequence
243 <220> FEATURE:
244 <223> OTHER INFORMATION: PCR primer
247 <221> NAME/KEY: misc_feature
248 <222> LOCATION: (1)...(17)
249 <223> OTHER INFORMATION: n = inosine
251 <400> SEQUENCE: 8
W--> 252 gtncknacrt cngcraartc                                        20
254 <210> SEQ ID NO: 9
255 <211> LENGTH: 1423
256 <212> TYPE: DNA
257 <213> ORGANISM: Phytophthora infestans
259 <220> FEATURE:
260 <221> NAME/KEY: CDS
261 <222> LOCATION: (2)...(1261)
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263 <400> SEQUENCE: 9
264 g atg gcg ata tcc cgc atg aaa gct gcg gcg atg gcg ctg cta cgt gcc 49
265   Met Ala Ile Ser Arg Met Lys Ala Ala Ala Met Ala Leu Leu Arg Ala
266   1           5                   10                  15
268 cgc cag acc tcc cag tcc gcc act caa cac ctc gcc ttc tct act gaa    97
269 Arg Gln Thr Ser Gln Ser Ala Thr Gln His Leu Ala Phe Ser Thr Glu
270             20                  25                  30
272 gcc act gat gct gca gct gcc gcg tta cgc atg ggc ttt aaa aag gct   145
273 Ala Thr Asp Ala Ala Ala Ala Ala Leu Arg Met Gly Phe Lys Lys Ala
274         35                  40                  45
276 cga aaa gac gag gat ggc ggt gtg aaa gtg ggg ctg gag gca gag ccc   193
277 Arg Lys Asp Glu Asp Gly Gly Val Lys Val Gly Leu Glu Ala Glu Pro
278     50                  55                  60
280 gat tca cca aca gat gtg agc gcc gtt tcg acg cca gta gta gag aag   241
281 Asp Ser Pro Thr Asp Val Ser Ala Val Ser Thr Pro Val Val Glu Lys
282 65                  70                  75                  80
284 aag ctc gtg ccg cca gcc atg agc tcc aca cag cca ctt tgg ctc aca   289
285 Lys Leu Val Pro Pro Ala Met Ser Ser Thr Gln Pro Leu Trp Leu Thr
286                 85                  90                  95
288 cag gac cat cct gtg aca gac ctg tcg ggc ttt gca ccg aag att gtg   337
289 Gln Asp His Pro Val Thr Asp Leu Ser Gly Phe Ala Pro Lys Ile Val
290             100                 105                 110
292 gtg gtt ggc gtc gga gga gct gga gga aat gcg gtg aac aac atg atc   385
293 Val Val Gly Val Gly Gly Ala Gly Gly Asn Ala Val Asn Asn Met Ile
294             115                 120                 125
296 gcg cgc ggc ctg cag ggt gtg gag ttt ctt gtt tgc aac acg gat gct   433
297 Ala Arg Gly Leu Gln Gly Val Glu Phe Leu Val Cys Asn Thr Asp Ala
298     130                 135                 140
300 cag cac tta cgc acg acg ctg acg gag aac cgc gtt cag atg gct cct   481
301 Gln His Leu Arg Thr Thr Leu Thr Glu Asn Arg Val Gln Met Ala Pro
302 145                 150                 155                 160
304 gaa ttg act gga gga ctg ggc tgt ggc gct aac ccc gaa gtt ggc cga   529
305 Glu Leu Thr Gly Gly Leu Gly Cys Gly Ala Asn Pro Glu Val Gly Arg
306                 165                 170                 175
308 gag gcg gca gag gcc gcg att gat gag att ttg gag cgc gtt cag ggt   577
309 Glu Ala Ala Glu Ala Ala Ile Asp Glu Ile Leu Glu Arg Val Gln Gly
310             180                 185                 190
312 gca aac atg atg ttt gtt act gcg ggt atg ggt ggc gga aca ggt aca   625
313 Ala Asn Met Met Phe Val Thr Ala Gly Met Gly Gly Gly Thr Gly Thr
314         195                 200                 205
316 ggt gca gca ccc gtc att gct cag gct gcc tta gat gct ggt atc ctc   673
317 Gly Ala Ala Pro Val Ile Ala Gln Ala Ala Leu Asp Ala Gly Ile Leu
318     210                 215                 220
320 acc gta gct gtc gtt act aag ccg ttc cgg ttt gag gga aac aac cgt   721
321 Thr Val Ala Val Val Thr Lys Pro Phe Arg Phe Glu Gly Asn Asn Arg
322 225                 230                 235                 240
324 gca aag ctt gcg gca caa ggc ctc gct gaa ctg aag gat agc gtc gat   769
325 Ala Lys Leu Ala Ala Gln Gly Leu Ala Glu Leu Lys Asp Ser Val Asp
326             245                 250                 255
```

VERIFICATION SUMMARY   DATE: 02/06/2001
PATENT APPLICATION: US/09/770,509   TIME: 15:23:10

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\02062001\I770509.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:220 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:236 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:252 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8